3. (Amended) The method as claimed in claim 1, characterized in that the mutation brings about a negligible reduction in the infectivity of the virus.

4. (Amended) The method as claimed in claim 1, characterized in that the mutated structural protein is capable of particle formation.

5. (Amended) The method as claimed in claim 1, characterized in that the mutated structural protein is capable of particle formation.

6. (Amended) The method as claimed in claim 1, characterized in that the structural protein is selected from mutated VP1, mutated VP2 and/or mutated VP3.

7. (Amended) The method as claimed in claim 1, characterized in that the structural protein is derived from AAV1, AAV2, AAV3, AAV4, AAV5 and/or AAV6 and other AAV serotypes derived therefrom, in particular from AAV2.

8. (Amended) The method as claimed in claim 1, characterized in that the mutation is a point mutation, a mutation of more than one amino acid, one or more deletion(s), in particular one or more insertion(s) or a combination of said modifications.

9. (Amended) The method as claimed in claim 1, characterized in that amino acids of a functional sequence which are preferably suitable for affinity chromatography are inserted.

10. (Amended) The method as claimed in claim 9, characterized in that the inserted amino acid sequence is selected from a ligand of a receptor or the receptor of a ligand, an antibody or part of an antibody, in particular an antibody epitope, an antigen or antigen epitope, a hormone, a hormone receptor, an enzyme, an enzyme substrate, a lectin, sugar-bearing amino acids, in particular from a histidine-rich peptide (His tag), a multiply charged peptide, glutathione S-transferase (GST tag), an F_c part of an antibody, an

immunoglobulin-binding domain, for example protein A or protein G or a part thereof, a lecitin, a nucleic acid binding site, a heparin binding site, a specific ligand, a specific receptor, an integrin, a cytokine or a receptor binding domain of a cytokine, integrin or growth factor, single-chain antibodies which bind to a cell surface receptor, an antibody against cell surface structures, an epitope and/or an antibody-binding structure.

11. (Amended) The method as claimed in claim 9, characterized in that a peptide which has the sequence QAGTFALRGDNPQG is inserted into said structural protein.

12. (Amended) The method as claimed in claim 1, characterized in that the structural protein comprises at least one other mutation.

13. (Amended) The method in claimed in claim 12, characterized in that the other mutation(s) brings about an alteration in the infectivity of the virus.

14. (Amended) The method as claimed in claim 12, characterized in that the other mutation(s) brings about a reduction in the antigenicity of the virus.

15. (Amended) The method as claimed in claim 12, characterized in that the other mutation(s) is/are one or more deletions(s), one or more insertion (s) or a combination of said modifications.

16. (Amended) The method as claimed in claim 15, characterized in that the insertion is a cell membrane receptor ligand, a Rep protein or peptide, an immunosuppressive protein or peptide and/or a protein or peptide with a signal for double strand synthesis of the foreign gene.

17. (Amended) The method as claimed in claim 15, characterized in that the insertion is selected from an integrin, a cytokine or a receptor binding domain of a cytokine, integrin or growth factor, single-chain antibodies which bind to a cell surface receptor, an antibody against cell surface structures, an antibody-binding structure or an epitope.

18. (Amended) The method as claimed in claim 1, characterized in that the mutation(s) is/are located on the virus surface.

19. (Amended) The method as claimed in claim 1, characterized in that the mutation(s) is/are located at the N terminus of the structural protein.

20. (Amended) The method as claimed in claim 1, characterized in that the mutation (s) is/are brought about by one or more insertions in the XhoI cleavage site of the VP1-encoding nucleic acid.

21. (Amended) The method as claimed in claim 1, characterized in that the mutation(s) is/are brought about by one or more insertions in the BsrBI cleavage site of the VP1-encoding nucleic acid.

22. (Amended) The method as claimed in claim 1, characterized in that the mutation (s) is/are brought about by one or more deletions between the BsrBI-HindII cleavage sites of the VP1-encoding nucleic acid and one or more insertions.

23. (Amended) The method as claimed in claim 1, characterized in that the mutation(s) is/are brought about by one or more deletions between the XhoI-XhoI cleavage sites of the VP1-encoding nucleic acid.

24. (Amended) The method as claimed in claim 1, characterized in that the mutation(s) is/are brought about by one or more deletions between the BsrBI-HindII cleavage sites of the VP1-encoding nucleic acid

25. (Amended) The method as claimed in claim 1, characterized in that one or more insertions in VP3 is/are located before and/or after at least one amino acid in the sequence selected from YKQIS SQSGA, YLTLN NGSQA, YYLSR TNTPS, EEKFF PQSGV, NPVAT EQYGS, LQRGN RQAAT, NVDFT VDTNG.